

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:31:55 ; Search time 13 Seconds
(without alignments)
79.762 Million cell updates/sec

Title: us-09-913-524-9
Perfect score: 143
Sequence: 1 PWSPALRLQRPPEPSAHAFCHR 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	143	100.0	366	1	IHA_RAT	P17490 rattus norv
2	140	97.9	366	1	IHA_MOUSE	O04957 mus musculu
3	131	91.6	265	1	IHA_SHEEP	P38440 ovis aries
4	131	91.6	360	1	IHA_BOVIN	P07994 bos taurus
5	131	91.6	367	1	IHA_HORSE	P55101 equus cabal
6	128	89.5	366	1	IHA_HUMAN	P05111 homo sapien
7	127	88.8	364	1	IHA_PIG	P04087 sus scrofa
8	120	83.9	361	1	IHA_TRITU	O77755 trichosurus
9	93	65.0	329	1	IHA_CHICK	P43031 gallus gall
10	54	37.8	2504	1	FAS_HUMAN	P49327 homo sapien
11	52.5	36.7	368	1	GP62_HUMAN	Q9b217 homo sapien
12	51	35.7	451	1	TBG1_HUMAN	P23258 homo sapien
13	51	35.7	451	1	TBG1_MOUSE	Q92310 mus musculu
14	51	35.7	451	1	TBG2_HUMAN	Q9a133 homo sapien
15	51	35.7	451	1	TBG2_MOUSE	Q9vck3 mus musculu
16	51	35.7	451	1	TBG_XENIA	P23330 xenopus lae
17	50	35.0	228	1	Z313_MOUSE	Q9et26 mus musculu
18	49	34.3	224	1	TIM4_MOUSE	Q9jhb3 mus musculu
19	49	34.3	228	1	Z313_HUMAN	O9y508 homo sapien
20	49	34.3	352	1	TPO_CANFA	P42705 canis famil
21	48.5	33.9	646	1	PIXB_HUMAN	Q14155 homo sapien
22	48.5	33.9	646	1	PIXB_RAT	O55043 rattus norv
23	48	33.6	192	1	NIF2_FRAAL	P46040 frankia aln
24	47.5	33.2	886	1	SM6B_MOUSE	O54951 mus musculu
25	47.5	33.2	887	1	SM6B_RAT	O70141 rattus norv
26	47	32.9	528	1	DRTS_DAUCA	P45350 daucus caro
27	47	32.9	622	1	BIN4_MOUSE	Q9z0h1 mus musculu
28	47	32.9	1122	1	HDA5_HUMAN	Q9uq16 homo sapien
29	47	32.9	1428	1	ATRN_MOUSE	O9wu60 mus musculu
30	47	32.9	1429	1	ATRN_HUMAN	O75882 homo sapien
31	47	32.9	1493	1	M3KL_MOUSE	P53349 mus musculu
32	46.5	32.5	391	1	NIRF_PSEST	O52521 pseudomonas
33	46.5	32.5	428	1	SYH_CHLMU	Q9pfj9 chlamydia m

RESULT 1

ID	IHA_RAT	STANDARD	PRT	366 AA
AC	P17490			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Inhibin alpha chain precursor.			
GN	INHA.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=90190649; PubMed-2628729;			
RA	Peng Z.-M., Li Y.-P., Chen C.-L.C.;			
RT	"Analysis of the 5'-flanking regions of rat inhibin alpha- and			
RT	beta-B-subunit genes suggests two different regulatory mechanisms.";			
RL	Mol. Endocrinol. 3:1914-1925(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91042598; PubMed=3153478;			
RA	Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;			
RT	"Rat inhibin: molecular cloning of alpha- and beta-subunit			
RT	complementary deoxyribonucleic acids and expression in the ovary.";			
RL	Mol. Endocrinol. 1:561-568(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90331931; PubMed 2484214;			
RA	Esch F.S., Shimazaki S., Cocksey K., Mercado M., Mason A.J.,			
RA	Ying S.Y., Dengo N., Ling N.;			
RT	"Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence			
RT	analysis of rat ovarian inhibins.";			
RL	Mol. Endocrinol. 1:388-396(1987).			
RN	[4]			
RP	TISSUE SPECIFICITY.			
RX	MEDLINE=88124801; PubMed-2829170;			
RA	Meunier H., Rivier C., Evans R.M., Vaie W.;			
RT	"Gonadal and extragonadal expression of inhibin alpha, beta A, and			
RT	beta B subunits in various tissues predicts diverse functions.";			
CC	Proc. Natl. Acad. Sci. U.S.A. 85:247-251(1988).			
CC	-!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,			
CC	RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.			
CC	INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE			
CC	FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,			
CC	GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,			
CC	ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,			
CC	EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR			
CC	SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF			
CC	ACTIVINS.			
CC	-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.			
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.			
CC	INHIBIN B IS A DIMER OF ALPHA AND BETA-B.			
CC	-!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN OVARY AND TESTIS. ALPHA-			

P13100 pneumocysti
O15213 homo sapien
P23799 trypanosoma
P10358 turnip yell
P20128 turnip yell
P28477 turnip yell
Q9es28 mus musculu
Q9h3t3 homo sapien
P19711 bovine vira
Q61337 mus musculu
O35147 rattus norv
P45351 cryptococcu

CC	AND BETA-B SUBUNIT IS ARE THE PREDOMINANT FORMS FOUND IN TESTIS.
CC	ALSO FOUND IN PLACENTA, PITUITARY, ADRENAL GLAND, BONE MARROW,
CC	KIDNEY, SPINAL CHORD AND BRAIN.
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
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CC	-----
DR	EMBL; M32755; AAA41437.1; -
DR	EMBL; M32754; AAA41437.1; JOINED.
DR	EMBL; M36453; AAA41435.1; -
DR	PIR; A40905; A40905.
DR	PIR; A41398; A41398.
DR	PIR; A40056; A40056.
DR	InterPro; IPR002405; Inhibin_alpha.
DR	InterPro; IPR001839; TGFb.
DR	Pfam; PF00019; TGF-beta; 1.
DR	PRINTS; PR00669; INHIBINA.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Growth factor; Hormone; Glycoprotein; Signal.
FT	SIGNAL 1 20
FT	PROPEP 21 233
FT	CHAIN 234 366
FT	DISULFID 263 328
FT	DISULFID 292 363
FT	DISULFID 296 365
FT	DISULFID 327 327
FT	CARBOHYD 147 147
FT	CARBOHYD 269 269
SQ	SEQUENCE 366 AA; 39496 MW; 327A23B9FEDFDC CRC64;
Query Mattr. 100.0%; Score 143; DB 1; Length 366;	
Best Local Similarity 100.0%; Pred. No. 9,6e-13;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 PWSPAALLRLQRPPEPSAHAFCHR 25
Db	241 PWSPAALLRLQRPPEPSAHAFCHR 265
RESULT 2	
IHA_MOUSE	
ID	IHA_MOUSE STANDARD; PRT; 366 AA.
QC	Q04997;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 1994, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Inhibin alpha chain precursor.
GN	INHA.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE=93321614; PubMed=8330535;
RA	Albano P.M., Groome N., Smith J.C.;
RT	"Activins are expressed in preimplantation mouse embryos and in ES
RT	and EC cells and are regulated on their differentiation.";
RL	Development 117:711-723(1993).
RN	[2]
RX	SEQUENCE FROM N.A.
RX	MEDLINE=92337610; PubMed=1632772;
RA	Su J.G.W., Hsueh A.J.W.;
RT	"Characterization of mouse inhibin alpha gene and its promoter.";
RT	Biochem. Biophys. Res. Commun. 186:283-300(1992).

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FT CHAIN 234 366 INHIBIN ALPHA CHAIN.
FT DISULFID 263 328 BY SIMILARITY.
FT DISULFID 292 363 BY SIMILARITY.
FT DISULFID 296 365 BY SIMILARITY.
FT DISULFID 327 327 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 165 165 A -> R (IN REF. 2).
FT CONFLICT 171 171 V -> G (IN REF. 2 AND 3).
FT CONFLICT 336 336 T -> R (IN REF. 2 AND 3).
SQ SEQUENCE 366 AA; 39536 MW; 8F3851B722FE0011 CRC64;

Query Match 97.9%; Score 140; DB 1; Length 366;
Best Local Similarity 96.0%; Pred. No. 2.5e-12;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPAALRLRLQRPPEPSAHAFCHR 25
Db 241 PWSPAALRLRLQRPPEPSAHAFCHR 265
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RESULT 3
IHA_SHEEP
ID IHA_SHEEP STANDARD; PRT; 265 AA.
AC P38440;
DT 01-OCT-1994 (Rel. 30, Created)
DI 01-OCT-1994 (Rel. 30, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain (Fragment).
GN INHA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 1;
RP SEQUENCE FROM N.A.
RC Tissue-Ovary.
RA Sadanandan S.L., Jeyaseelan K.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOPHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL; I28815; AAA31553.1; -
CC InterPro; IPR001839; TGFb.
CC Pfam; PF00019; TGF-beta; 1.
CC ProDom; PD000357; TGFb; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Hormone; Glycoprotein.
CC NON_TER 1
FT DISULFID 161 227 BY SIMILARITY.
FT DISULFID 190 262 BY SIMILARITY.
FT DISULFID 194 264 BY SIMILARITY.

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FT DISULFID 226 226 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 265 AA; 28754 MW; D880E9AB156B656 CRC64;

Query Match 91.6%; Score 131; DB 1; Length 265;
Best Local Similarity 92.0%; Pred. No. 3.2e-11;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPAALRLRLQRPPEPSAHAFCHR 25
Db 139 PWSPAALRLRLQRPPEPSAHAFCHR 163
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RESULT 4
IHA_BOVIN
ID IHA_BOVIN STANDARD; PRT; 360 AA.
AC PC7594;
DT 01-AUG-1988 (Rel. 08, Created)
DI 01-AUG-1988 (Rel. 08, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1;
RP SEQUENCE FROM N.A.
RC Tissue-Follicular fluid;
RC MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wettinball R.E.H., Burger H.G., de Kretser D.M.;
RT "Cloning and sequence analysis of cDNA species coding for the two
RT subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RN 12;
RP SEQUENCE OF 1-87 FROM N.A.
RC Tissue=Liver;
RC MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Grouin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting.";
RL Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOPHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; M13273; AAA97414.1; -
CC EMBL; A14416; CAA01156.1; -
CC EMBL; U16237; AAB60262.1; -

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EMBL; D50327; BAA08863.1; -;
EMBL; U21219; AAB00874.1; -;
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFbeta
Pfam; PF000019; TGF-beta; 1.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGF8; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 233 BY SIMILARITY.
FT CHAIN 234 329 INHIBIN ALPHA CHAIN.
FT DISULFID 263 329 HY SIMILARITY.
FT DISULFID 292 364 BY SIMILARITY.
FT DISULFID 296 366 BY SIMILARITY.
FT DISULFID 328 328 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 147 147 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 105 105 Q > R (IN REF. 2).
FT CONFLICT 171 171 G > R (IN REF. 2).
FT CONFLICT 176 176 C > R (IN REF. 2).
SQ SEQUENCE 367 AA; 39422 MW; DC8A6E2C04B2C61 CMK64;

Query Match 91.6%; Score 131; DB 1; Length 367;
Best Local Similarity 92.0%; Pred. No. 4.5e-11;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPAALRLQLRPPEPSAHAFCHR 25
DB 241 PWSPAALRLQLRPPEPSAHANCHR 265

RESULT 6
IHA_HUMAN
ID IHA_HUMAN STANDARD; PRT; 366 AA.
AC P05111;
DT 13-AUG-1987 (Rel. 05, Created)
DD 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Felidae; Mustelidae; Mustelinae; Haplorhini; Platyrrhini; Simiiformes; Hominoidea; Hominidae; Hominini; Homo.
OX NCBI_TaxId=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=86287450; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.G..
EV Evans R.M., Vale W.;
RT "Inhibin A-subunit cDNAs from porcine ovary and human placenta.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RN [2]
RS SEQUENCE FROM N.A.
RX MEDLINE=87005283; PubMed=3758355;
RA Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage k.G.;
EV "Human inhibin genes: genomic characterisation and sequencing.";
RL FEBS Lett. 206:329-334(1986).
RN [3]
RS SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RS SEQUENCE OF 16-366 FROM N.A.
RX MEDLINE=86186863; PubMed=3754442;
RA

RA Mason A.J., Niall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
RN [15]
RP TISSUE SPECIFICITY, AND INDUCTION.
RX MEDLINE: 98165602; PubMed: 9506758;
RA Mellor S.L., Richards M.G., Pedersen J.S., Robertson D.M.,
KA Risbridger G.P.;
RT "Loss of the expression and localization of inhibin alpha-subunit in
RT high grade prostate cancer";
RL J. Clin. Endocrinol. Metab. 83:969-975(1998).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- TISSUE SPECIFICITY: ORIGINALLY FOUND IN OVARY (GRANULOSA CELLS)
CC AND TESTIS (SEBTOLI CELLS) BUT IT IS WIDELY DISTRIBUTED IN MANY
CC TISSUES INCLUDING BRAIN AND PLACENTA. IN ADRENAL CORTEX EXPRESSION
CC IS LIMITED TO THE ZONA RETICULARIS AND THE INNERMOST ZONA
CC FASCICULATA IN THE NORMAL GLAND, EXTENDING CENTRIPETALLY INTO THE
CC ZONA FASCICULATA IN HYPERPLASIA. ALSO FOUND IN ADRENOCORTICAL
CC TUMORS. ALSO EXPRESSED IN PROSTATE EPITHELIUM OF BENIGN PROSTATIC
CC HYPERPLASIA, IN REGIONS OF BASAL CELL HYPERPLASIA AND IN
CC NONMALIGNANT REGIONS OF HIGH GRADE PROSTATE CANCER. ONLY
CC CIRCULATING INHIBIN B IS FOUND IN MALE, WHEREAS CIRCULATING
CC INHIBINS A AND B ARE FOUND IN FEMALE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL: M1981; AAA59166.1; -
CC EMBL: M1344; AAA59167.1; -
CC EMBL: BC006391; AAH06391.1; -
CC EMBL: X0445; CAA28040.1; -
CC EMBL: X0446; CAA28040.1; JOINED.
CC EMBL: A14420; CAA01158.1; -
CC PIR: A23556; A23556.
CC PIR: A24248; A24248.
CC PIR: B25947; B25947.
CC Genew: HGNC:6065; INHA.
CC MIM: 147380; -
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.
CC Pfam: PF00019; TGF-beta; 1.
CC PRINTS: PR00669; INHIBINA.
CC PRODOM: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 18
FT PROPEP 19 232
FT CHAIN 233 366
FT DISULFID 262 328
FT DISULFID 291 363
FT DISULFID 295 365
FT DISULFID 327 327
FT CARBOHYD 146 146
FT CARBOHYD 268 268
FT CARBOHYD 302 302

FT CONFLICT 17 17 H -> V (IN REF. 4).
RT CONFLICT 19 19 C -> S (IN REF. 4).
SQ SEQUENCE 366 AA; 39669 MW; 0E03D2AB12BF8E57 CRC64;
Query Match 89.5%; Score 128; DB 1; Length 366;
Best Local Similarity 88.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 PWSPALRLQLRPPPEPSAHAFCHR 25
IIII:IIIIIIIIII:IIII
DB 240 PWSPALRLQLRPPPEPSAHAFCHR 264
RESULT 7
IHA_PIG STANWARD; PRT; 364 AA.
AC P04087;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86287350; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.G.,
RA Evans R.M., Vale W.;
RT "Inhibin A-subunit cDNAs from porcine ovary and human placenta.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 231-256.
RC TISSUE-Ovarian follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RT factor-beta";
RL Nature 318:659-663(1985).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL: M13980; AAA31057.1; -
CC EMBL: X03265; CAA27019.1; -
CC PIR: A01392; WPPGA.
CC PIR: A25947; A25947.
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.
CC Pfam: PF00019; TGF-beta; 1.
CC PRINTS: PR00669; INHIBINA.

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DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 230 INHIBIN ALPHA CHAIN.
FT CHAIN 231 364 BY SIMILARITY.
FT DISULFID 260 326 BY SIMILARITY.
FT DISULFID 289 361 BY SIMILARITY.
FT DISULFID 293 363 BY SIMILARITY.
FT DISULFID 325 325 INTERCHAIN (BY SIMILARITY).
FT DISULFID 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 R -> H (IN REF. 2).
FT CONFLICT 125 125 A -> T (IN REF. 2).
SQ SEQUENCE 364 AA; 39160 MW; BB595B9B7958A168 CRC64;

Query Match 88.8%; Score 127; DB 1; Length 364;
Best Local Similarity 88.0%; Pred. No. 1.6e-10;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PWSPALRLQLRPPEPSAHAFCHR 25
| | | | | | | | | | | | | | | | | | | | |
DB 238 PWSPALRLQLRPPEPSAHAFCHR 262

RESULT 8
IHA_TRIVU
ID IHA_TRIVU STANDARD; PRI; 361 AA.
AC 077755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID:9337;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:99027340; PubMed:9801457;
RA Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
RA Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of
RT the inhibin alpha subunit of Australian brushtail possum (Trichosurus
RT vulpecula).";
RL J. Mol. Endocrinol. 21:141-152(1998).
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to licensee@isb-sib.ch).
CC -----
CC EMBL: AF033340; AAC63945.1;
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.

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DR PFAM: PF00019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 230 BY SIM. ARITY.
FT CHAIN 231 361 INHIBIN ALPHA CHAIN.
FT DISULFID 260 323 BY SIMILARITY.
FT DISULFID 289 358 BY SIMILARITY.
FT DISULFID 293 360 BY SIMILARITY.
FT DISULFID 322 322 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAA87D CRC64;

Query Match 83.9%; Score 120; DB 1; Length 361;
Best Local Similarity 84.0%; Pred. No. 1.5e-09;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PWSPALRLQLRPPEPSAHAFCHR 25
| | | | | | | | | | | | | | | | | | | | |
DB 238 PWSPALRLQLRPPEPSAHAFCHR 262

RESULT 9
IHA_CHICK
ID IHA_CHICK STANDARD; PRI; 329 AA.
AC P43031; Q90708;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin alpha chain precursor.
GN INHA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID:9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-White leghorn; TISSUE-Ovarian granulosa;
RX MEDLINE:94002740; PubMed:8399835;
RA Wang S.Y., Johnson P.A.;
RT "Complementary deoxyribonucleic acid cloning and sequence analysis of
RT the alpha-subunit of inhibin from chicken ovarian granulosa cells.";
RL Biol. Reprod. 49:453-458(1994).
RN [2]
RP REVISIONS.
RC STRAIN-White leghorn;
RC Johnson P.A., Chen C.C.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL: AF033340; AAC63945.1;
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.

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CC -----
 DR EMBL: U48438; AAA92569.1; -.
 DR HSPSP; P18075; 1BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: P000669; INHIBINA.
 DR PRODOM: P000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF.BETA.1; 1.
 KW Growth factor; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 216 POTENTIAL.
 FT CHAIN 217 329 INHIBIN ALPHA CHAIN.
 FT DISULFID 242 291 BY SIMILARITY.
 FT DISULFID 271 326 BY SIMILARITY.
 FT DISULFID 275 328 BY SIMILARITY.
 FT DISULFID 290 290 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 329 AA; 35853 MW; AE331687109A25A1 CRC64;
 Query Match 65.0%; Score 93; DB 1; Length 329;
 Best Local Similarity 68.0%; Pred. No. 8e-06; Mismatches 2; Indels 0; Gaps 0;
 Matches 17; Conservative 2;
 Qy 1 PWSPAALRIQLRPPEPSAHAFCHR 25
 ||||| ||||| : ||| |
 Db 220 PWSPAALSLQLRPSEDVAHNCRR 244
 RESULT 10
 FAS_HUMAN
 ID FAS_HUMAN STANDARD; PRT; 2504 AA.
 AC P49327;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fatty acid synthase (EC 2.3.1.85) [includes: EC 2.3.1.38; EC 2.3.1.39;
 DE EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14].
 GN FASN OR FAS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96004605; PubMed=7567999;
 RA Jayakumar A., Tai M.-H., Huang W.-Y., Al-Feel W., Hsu M.,
 RA Abu-Elheiga L., Chirala S.S., Wakil S.J.;
 RT "Human fatty acid synthase: properties and molecular cloning";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:8695-8699(1995).
 RN [2]
 RP SEQUENCE OF 753-758 AND 1285-1297.
 RX MEDLINE=94294385; PubMed=8022791;
 RA Kuhnaja F.P., Jenner K., Wood F.D., Hennigar R.A., Jacobs L.B.,
 RA Dick J.D., Pasternack G.R.;
 RT "Fatty acid synthesis: a potential selective target for
 RT antineoplastic therapy";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6379-6383(1994).
 CC -!- FUNCTION: FATTY ACID SYNTHASE CATALYZES THE FORMATION OF
 CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 CC THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES AND AN
 CC ACYL CARRIER PROTEIN.
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
 CC long-chain fatty acid + (N+1) CoA + N Co(2) + 2N NADP(+).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + [acyl-carrier protein] = CoA +
 CC acetyl-[acyl-carrier protein].
 CC -!- CATALYTIC ACTIVITY: Malonyl-CoA + [acyl-carrier protein] = CoA +
 CC malonyl-[acyl-carrier protein].

CC -!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
 CC [acyl-carrier protein].
 CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxypalmitoyl-[acyl-carrier protein]
 CC = 2-hexadecenoyl-[acyl-carrier protein] + H(2)O.
 CC -!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
 CC -!- CATALYTIC ACTIVITY: Oleoyl-[acyl-carrier protein] + H(2)O = [acyl-
 CC carrier protein] + oleate.
 CC -!- SUBUNIT: HOMODIMER, WHICH IS ARRANGED IN A HEAD TO TAIL FASHION.
 CC -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN BRAIN, LUNG, AND
 CC LIVER.
 CC -!- MISCELLANEOUS: THE RELATIVELY LOW BETA-KETOACYL SYNTHASE ACTIVITY
 CC MAY BE ATTRIBUTABLE TO THE LOW --PHOSPHOPANTHETHEINE CONTENT OF
 CC THE PROTEIN.
 CC -----
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 CC -----
 CC EMBL: U26644; AAC50259.1; -.
 CC Genew; HGNC:3594; FASN.
 DR MIN: 600212; .
 DR InterPro: IPR001227; Ac-transferase.
 DR InterPro: IPR002085; Adh_zn_family.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Pantne_attach.
 DR InterPro: IPR000051; SAM_bind.
 DR InterPro: IPR001031; Thioesterase.
 DR Pfam: PF00107; adh_zinc; 1.
 DR Pfam: PF00109; ketoacyl-synt; 1.
 DR Pfam: PF00550; pp-binding; 1.
 DR Pfam: PF00698; Acyl_transf; 1.
 DR Pfam: PF00975; Thioesterase; 1.
 DR Pfam: PF02801; ketoacyl-synt-C; 1.
 DR PROSITE: PS00606; B-KETOACYL-SYNTHASE; 1.
 DR PROSITE: PS50075; ACP_DOMAIN; 1.
 DR Fatty acid biosynthesis; Multifunctional enzyme; Phosphopantetheine;
 KW Hydroxylase; Oxidoreductase; Transferase; Lyase; NADP;
 KW Pyridoxal phosphate.
 FT DOMAIN 1 413 BETA-KETOACYL SYNTHASE.
 FT DOMAIN 428 815 ACYL AND MALONYL TRANSFERASES.
 FT DOMAIN 1630 1857 ENOYL REDUCTASE.
 FT DOMAIN 1858 2113 BETA-KETOACYL REDUCTASE.
 FT DOMAIN 2118 2174 ACYL CARRIER (ACP).
 FT DOMAIN 2202 2504 THIOESTERASE.
 FT ACT_SITE 161 161 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT ACT_SITE 580 580 MALONYLTRANSFERASE (BY SIMILARITY).
 FT ACT_SITE 876 876 BETA-HYDROXYACYL DEHYDRATASE (BY
 FT SIMILARITY).
 FT NP_BIND 1666 1683 NADP (ER).
 FT BINDING 1699 1699 PYRIDOYL PHOSPHATE (BY SIMILARITY).
 FT NP_BIND 1880 1895 NADP (KR).
 FT BINDING 2151 2151 PHOSPHOPANTHETHEINE (BY SIMILARITY).
 FT ACT_SITE 2302 2302 THIOESTERASE (BY SIMILARITY).
 FT ACT_SITE 2475 2475 THIOESTERASE (BY SIMILARITY).
 SQ SEQUENCE 2504 AA; 273100 MW; 8AAF9809B2738DFA CRC64;
 Query Match 37.8%; Score 54; DB 1; Length 2504;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 9 LLORPPEPSAHAF 22
 ||: ||||: ||||
 Db 1514 LLEDKPEPTAHAF 1527

RESULT 11

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GP62_HUMAN          STANDARD:          PRT:    368 AA.
ID   GP62_HUMAN
AC   Q9BZJ7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Probable G protein-coupled receptor GPR62.
GN   GPR62.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE-21105113; PubMed-11165367;
RA   Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
RA   Lynch K.R., O'Dowd B.F.;
RT   Identification of four novel human G protein-coupled receptors
RT   expressed in the brain.; 86:13-22(2001).
RL   Brain Res. Mol. Brain Res. 86:13-22(2001).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in brain; detected in the basal
CC   forebrain, frontal cortex, caudate, putamen, thalamus and
CC   hippocampus.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL: AF317653; AAK12638.1; -
DR   Genew; HGNC:13301; GPR62.
DR   MIM: 606917; -
DR   InterPro: IPR000276; GPCR_Rhodpsn.
DR   Pfam: PF00001; 7tm_1; 1.
DR   PRINTS: PR00237; GPCRHHODPSN.
DR   PROSITE: PS00237; G-PROTEIN-RECEP_F1_1; FALSE_NEG.
DR   PROSITE: PS00266; G-PROTEIN-RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN          1   18   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        19   39   1 (POTENTIAL).
FT   DOMAIN          40   53   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM        54   74   2 (POTENTIAL).
FT   DOMAIN          75   91   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        92   112   3 (POTENTIAL).
FT   DOMAIN          113   129   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM        130   150   4 (POTENTIAL).
FT   DOMAIN          151   177   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        178   198   5 (POTENTIAL).
FT   DOMAIN          199   239   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM        240   260   6 (POTENTIAL).
FT   DOMAIN          261   272   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        273   293   7 (POTENTIAL).
FT   DOMAIN          294   368   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN          239   285   ALA-RICH.
FT   CARBOHYD         3     3   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD         8     8   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE 368 AA; 37628 MW; 9CFF95298012C75 CRC64;
```

Query Match 36.7%; Score 52.5; DB 1; Length 368;

Best local Similarity 61.1%; Pred No. 4;

Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 WSP-AALRLQLRPPPEPS 18

I I I I I I I I I I

Db 321 WHPRALLQLRPPPEGPA 338

```
RESULT 12
TBG1_HUMAN          STANDARD:          PRT:    451 AA.
ID   TBG1_HUMAN
AC   P23258; Q9BW59;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex
DE   component 1) (GCP-1).
GN   TUBG1 OR TUBG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE-91249388; PubMed-1904010;
RA   Zheng Y., Jung M.K., Oakley B.R.;
RT   "Gamma-tubulin is present in Drosophila melanogaster and Homo sapiens
RT   and is associated with the centrosome.";
RL   Cell 65:817-823(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE-Skin;
RA   Strausberg R.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DOBJ databases.
RN   [3]
RP   MASS SPECTROMETRY.
RC   TISSUE-Breast Cancer;
RX   MEDLINE-21829512; PubMed-11840567;
RA   Hartis R.A., Yang A., Stein K.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [4]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE-98234404; PubMed-9566969;
RA   Tassin A.-M., Celati C., Moudjou M., Borneus M.;
RT   "Characterization of the human homologue of the yeast spe98p and its
RT   association with gamma-tubulin.";
RL   J. Cell Biol. 141:689-701(1998).
CC   -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC   SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC   IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC   -!- SUBUNIT: Interacts with GTP2 and GCP3.
CC   -!- SUBCELLULAR LOCATION: Centrosome.
CC   -!- MASS SPECTROMETRY: MW=51197.98; METHOD MALDI.
CC   -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL: M61764; AAA52620.1; -
DR   EMBL: BC000619; AAH00619.1; -
DR   PIR: A39527; UBHUG.
DR   Genew; HGNC:12417; TUBG1.
DR   MIM: 191135; -
DR   InterPro: IPR000217; Tubulin.
DR   InterPro: IPR003008; Tubulin_Fts2.
DR   Pfam: PF00091; tubulin; 1.
DR   PRINTS: PR01161; TUBULIN.
DR   PROSITE: PS00227; TUBULIN; 1.
KW   Microtubules; GTP-binding.
NP_BIND 142 148 GTP (POTENTIAL).
```


FT CONFLICT 35 35 G -> A (IN REF. 1).
ST CONFLICT 202 202 V -> L (IN REF. 1).
SQ SEQUENCE 451 AA: 51170 MW; E2A4C0179ED0CFE8 CRC64;

Query Match 35.7%; Score 51; DB 1; Length 451;
Best Local Similarity 45.5%; Pred. No. 8.2;
Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PWSAALR--LLQRPPEPSAH 20

||||: ||: | ||||

Db 350 PWGPASIQVALSRKSPYLPSAH 371

RESULT 13

TBG1_MOUSE

ID TBG1_MOUSE STANDARD; PRT; 451 AA.

AC Q9Z310;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex

DE component 1) (GCP-1).

GN TBG1 OR TUBG.

OS Mus musculus (Mouse), and

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090, 10116;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES-Mouse;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES-Rat;

RX MEDLINE=99397453; PubMed=10470852;

RA Nakadai T., Okada N., Makino Y., Tamura T.;

RI "Structure of rat gamma-tubulin and its binding to HP33.";

RL DNA Res. 6:207-209(1999).

CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT

CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA

CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN (BY

CC SIMILARITY).

CC -!- SUBUNIT: Interacts with GCP2 and GCP3 (By similarity).

CC -!- SUBCELLULAR LOCATION: Centrosome (By similarity).

CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; H006581; AA06581.1; -;

DR EMBL; AB015946; BAA36504.1; -;

DR MGDB; MG1-101834; Tuba9

DR InterPro; IPR000217; Tubulin.

DR InterPro; IPR003008; Tubulin_Pts2.

DR Pfam; PF00091; tubulin; 1.

DR PRINTS; PR01161; TUBULIN.

DR PROSITE; PS00227; TUBULIN; 1.

KW Microtubules; GTP-binding.

FT NP_BIND 142 148 GTP (POTENTIAL).

SQ SEQUENCE 451 AA: 51100 MW; A8F106BD12D0C88A CRC64;

Query Match 35.7%; Score 51; DB 1; Length 451;
Best Local Similarity 45.5%; Pred. No. 8.2;
Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PWSAALR--LLQRPPEPSAH 20

||||: ||: | ||||

Db 350 PWGPASIQVALSRKSPYLPSAH 371

RESULT 14

TBG2_HUMAN

ID TBG2_HUMAN STANDARD; PRT; 451 AA.

AC Q9NRH3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE tubulin gamma-2 chain (Gamma-2 tubulin).

GN TUBG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20366133; PubMed=10903841;

RA Wise D.O., Krahe R., Oakley B.R.;

RT "The gamma-tubulin gene family in humans.";

RL Genomics 67:164-170(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Mammary gland;

RA Isogai T., Ota T., Hayashi K., Sujiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Ninomiya K., Iwayanagi T.;

RT "NEO human cDNA sequencing project.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.

CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)

CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT

CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.

CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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DR EMBL; AF225971; AAF34188.1; -;

DR EMBL; AK022324; BAB14012.1; -;

DR EMBL; BC009670; AA09670.1; -;

DR Genew; HGNC:12419; TUBG2.

DR MIM; 605785; -;

DR InterPro; IPR000217; Tubulin.

DR InterPro; IPR003008; Tubulin_Pts2.

DR Pfam; PF00091; tubulin; 1.

DR PRINTS; PR01161; TUBULIN.

DR PROSITE; PS00227; TUBULIN; 1.

KW Microtubules; GTP-binding.

FT NP_BIND 142 148 GTP (POTENTIAL).

SQ SEQUENCE 451 AA: 51091 MW; FDE2CB5A33D92691 CRC64;

Query Match 35.7%; Score 51; DB 1; Length 451;
Best Local Similarity 45.5%; Pred. No. 8.2;
Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PWSAALR--LLQRPPEPSAH 20

```

Db 350 FWGPASIQVALSRKSPYLP5AH 371
      |||::: |::| ||||
RESULT 15
TBG2_MOUSE
ID TBG2_MOUSE STANDARD; PRT: 451 AA.
AC Q8VCK3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tubulin gamma-2 chain (Gamma-2 tubulin).
GN TBG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: B019652; AAB19652.1; -.
DR InterPro: IPR000217; Tubulin.
DR InterPro: IPR003008; Tubulin_FtsZ.
DR PROSITE: PS00227; TUBULIN; 1.
KW Microtubules; GTP-binding.
FT NP_BIND 142 148 GTP (POTENTIAL).
SQ SEQUENCE 451 AA; 51121 MW; 1FC0CFE1E04839AA CRC64;

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Query Match 35.7%; Score 51; DR 1; Length 451;
Best local Similarity 45.5%; Pred. No. 8.2;
Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;
QY 1 FWGPASLR-LIQRPPEPSAH 20
      |||::: |::| ||||
Db 350 FWGPASIQVALSRKSPYLP5AH 371

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Job time : 13 secs